## 1 DT12 Rec'd PCT/PTO 2 9 NOV 2004

## SEQUENCE LISTING

<110	)> St	ınGei	ne Gi	nbH &	Co.	KGa <i>l</i>	Ą								٠	
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<130	)> PI	5368	37		•			•				٠				
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tca Ser	tta Leu	tgc Cys	atc Ile 20	tca Ser	tgc Cys	cag Gln	caa Gln	gcc Ala 25	ttc Phe	ggt Gly	acg Thr	caa Gln	caa Gln 30	ccc Pro	ttg Leu	96
				agt Ser												144
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tat Tyr	cta Leu	aaa Lys	gcc Ala	ttg Leu .85	Gly ggg	att Ile	gat Asp	gcc Ala	att Ile 90	tgg Trp	atc Ile	aac Asn	cca Pro	cat His 95	tat Tyr	288
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				tat Tyr												384
				cgg Arg												432
				caa Gln												480
				cgc Arg 165												528

cag gcg cct aat aat tac cct tca ttc ttt ggt ggc tcg gcg tgg caa 576 Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln aaa gat gaa aag acc aat caa tac tac ctg cac tat ttt gct aaa caa 624 Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln cag cct gac cta aac tgg gat aat ccc aaa gtc cgt caa gat ctt tat 672 Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr 210 gca atg tta cgt ttc tgg tta gat aaa ggc gtg tct ggt tta cgt ttt 720 Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe 225 230 235 gat acg gta gcg acc tac tca aaa att ccg gat ttc cca aat ctc acc 768 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr 245 caa caa cag ctg aag aat ttt gca gcg gag tat acc aag ggc cct aat 816 Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn 260 265 att cat cgt tac gtc aat gaa atg aat aaa gag gtc ttg tct cat tac 864 Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr 280 gac att gcg act gcc ggt gaa atc ttt ggc gta ccc ttg gat caa tcg 912 Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser 295 ata aag ttc ttc gat cgc cgc cgt gat gag ctq aac att gca ttt acc 960 Ile Lys Phe Phe Asp Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr 310 315 ttt gac tta atc aga ctc gat cga gac tct gat caa aga tgg cgt cga 1008 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg aaa gat tgg aaa ttg tcg caa ttc cgg cag atc atc gat aac gtt gac 1056 Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp 340 cgt act gca gga gaa tat ggt tgg aat gcc ttc ttc ttg gat aac cac 1104 Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His 355 gac aat ccg cgc gct gtc tcg cac ttt ggc gat gat gat cgc cca caa 1152 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Asp Pro Gln 370 375 tgg cgt gag cca tcg gct aaa gcg ctt gca acc ttg acg ctg act caa 1200 Trp Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln 390 395 cga gca aca cct ttt att tat caa ggt tca gaa ttg ggc atg acc aat 1248 Arg Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn 410 tac ccg ttt aaa gct att gat gaa ttc gat gat att gag gtg aaa ggt 12.96 Tyr Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly 425 ttt tgg cat gac tac gtt gag aca gga aag gtc aaa gcc gac gag ttc 1344 Phe Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe 435

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Phe Lys Val		Tyr Gln Glu	Ile Asn Ala	Val Ser Gln Val	
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Thr Gln Pro			Tyr Arg Gln	Leu Ile Lys Ile	
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		_		Thr Asp Leu Asp	
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Lys Tyr Leu 545		Asn Phe Lys		Met Arg Tyr Lys	
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Leu Pro Asp	Asn Leu Ser 565	Ile Glu Lys		Asp Ser Asn Ser	
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Phe Phe Ser				103	, ,
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	Lys Ser Ile	Glu Gln Ser	Lys Thr Ile	Pro Lys Trp Trp	
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Lys Glu Ala	Val Phe Tyr	Gln Val Tyr	Pro Arg Ser	Phe Lys Asp Thr	
50		55	60		
Asn Gly Asp	Gly Ile Gly	Asp Ile Asn	Gly Ile Ile	Glu Lys Leu Asp	
65	70		75	80	
			•		

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	Glu	Met 130	Lys	Lys	Arg	Asn	Met 135	Arg	Leu	Met	Ile	Asp 140	Val	Val	Ile	Asn
	His 145	Thr	Ser	Asp	Gln	Asn 150	Glu	Trp	Phe	Vạl	Lys 155	Ser	Lys	Ser	Ser	Lys 160
	Asp	Asn	Pro	Tyr	Arg 165	Gly	Tyr	Tyr	Phe	Trp 170	Lys	Asp	Ala	Ļys	Glu 175	Gly
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	Ala 225	Met	Leu	Arg	Phe	Trp 230	Leu	Asp	Lys	Gly	Val 235	Ser	Gly	Leu	Arg	Phe 240
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	Ile	His	Arg 275	Tyr	Val	Asn	Glu	Met 280	Asn	Lys	Glu	Val	Leu 285	Ser	His	Tyr
	Asp	Ile 290	Ala	Thr	Ala	Gly	Glu 295	Ile	Phe	Gly	Val	Pro 300	Leu	Asp	Gln	Ser
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	Phe	Asp	Leu	Ile	Arg 325	Leu	Asp	Arg	Asp	Ser 330	Asp	Gln	Arg	Trp	Arg 335	Arg
	Lys	Asp	Trp	Lys 340	Leu	Ser	Gln	Phe	Arg 345	Gln	Ile	Ile	Asp	Asn 350	Val	Asp
	Arg	Thr	Ala 355	Gly	Glu	Tyr	Gly	Trp 360	Asn	Ala	Phe	Phe	Leu 365	Asp	Asn	His
		370				Val	375					380				
	Trp 385	Arg	Glu	Pro	Ser	Ala 390	Lys	Ala	Leu	Ala	Thr 395	Leu	Thr	Leu	Thr	Gln 400
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	Tyr	Pro	Phe	Lys 420	Ala	Ile	Asp	Glu	Phe 425	Asp	Asp	Ile	Glu	Val 430	Lys	Gly
			4.35			Val		440					445		•	
	Leu	Gln. 450	Asn.	Val	Arg	Leu	Thr 455	Ser	Arg	Asp	Asn	Ser 460	Arg	Thr	Pro	Phe
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Gln Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp 475 Phe Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Thr Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile 505 Arg His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp 520 ' Pro Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys 550 555 Leu Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser 570 Lys Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp 580 585 Gln Ser Gly Val Tyr Lys Thr Lys Ser Ile Asn Leu Ile Val Thr Pro Asn Asn Val Asn Ile Leu Lys Leu Leu Lys Pro Ala Phe Tyr Ala Gly 615 620 Phe Phe Ser Ala Lys 625 <210> 3 <211> 1305 <212> DNA <213> Erwinia rhapontici <220> <221> CDS <222> (1)..(1305) <223> coding for N-terminal fragment of sucrose isomerase <400>. 3 atg tcc tct caa gga ttg aaa acg gct ntc gct att ttt ctt gca acc Met Ser Ser Gln Gly Leu Lys Thr Ala Xaa Ala Ile Phe Leu Ala Thr act ttt tct gcc aca tcc tat cag gcc tgc agt gcc nnn cca gat acc 96 Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Xaa Pro Asp Thr 20 gcc ccc tca ctc acc gtt cag caa tca aat gcc ctg ccc aca tqq tqq Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp aag cag gct gtt ttt tat cag gta tat cca cgc tca ttt aaa gat acg 192 Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr 55 aat ggg gat ggc att ggg gat tta aac ggt att att gag aat tta gac Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp 70 tat ctg aag aaa ctg ggt att gat gcg att tgg atc aat cca cat tac 288 Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr

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		ccg Pro														336
		aaa Lys 115														384
		aag Lys														432
cac His 145	acc Thr	agc Ser	gat Asp	cag Gln	cat His 150	gcc Ala	tgg Trp	ttt Phe	gtt Val	cag Gln 155	agc Ser	aaa Lys	tcg Ser	ggt Gly	aag Lys 160	480
		ccc Pro														528
		ccc Pro														576
		gat Asp 195														624
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		ctc Leu														720
		gtt Val														768
		cag Gln														816
		gac Asp 275														864
gat Asp	atc Ile 290	gcc Ala	act Thr	gcg Ala	gly	gaa Glu 295	ata Ile	ttt Phe	ggg Gly	gtt Val	cct Pro 300	ctg Leu	gat Asp	aaa Lys	tcg Ser	912
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ttt Phe	gat Asp	ctg Leu	atc Ile	agg Arg 325	ctc Leu	gat Asp	cgt Arg	gat Asp	gct Ala 330	gat Asp	gaa Glu	aga Arg	tgg Trp	cgg Arg 335	cga Arg	1008
		tgg Trp														1056
caa Gln	acg Thr	gca Ala 355	gga Gly	gag Glu	tat Tyr	ggg Gly	tgg Trp 360	aat Asn	gcc Ala	ttt Phe	ttc Phe	tta Leu 365	gac Asp	aat Asn	cac His	1104

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cgc Arg 385	gag Glu	cat His	gcg Ala	gcg Ala	aaa Lys 390	gca Ala	ctg Leu	gca Ala	aca Thr	ttg Leu 395	acg Thr	ctg Leu	acc Thr	cag Gln	cgt Arg 400	1200
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CCC	ttt Phe	aaa Lys	aaa Lys 420	atc Ile	gat Asp	gat Asp	ttc Phe	gat Asp 425	gat Asp	gta Val	gag Glu	gtg Val	aaa Lys 430	ggt Gly	ttt Phe	1296
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Thr	Phe	Ser	Ala	Thr	Ser	Туг	Gln	λla		802	ח ה	Vaa	Dro		mh	
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Ala	Pro	Ser 35	Leu	Thr	Val	Gln	Gln 40	Ser	Asn	Ala	Leu	Pro 45		Trp	Trp	÷
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145					His 150			,		155				_	160	
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•			18.0		Tyr			185					190			•
Lys	Asp	Asp 195	Lys	Ser	Gly	Gln	Tyr 200	Tyr	Leu	His	Tyr	Phe 205	Ala	Lys	Gln	
Gln	Pro 21.0.	Asp	Leu	Asn	Trp	Asp 215	Asn	Pro	Lys	Val	Arg 220	Gln	Asp	Leu	Tyr	
Asp 225	Met	Leu	Arg	Phe	Trp 230	Leu	Asp	Lys	Gly	Val 235	Ser	Gly	Leu	Arg	Phe 240	

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													cgt Arg		336
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	-		-		_	_	_	_	-		_	_	atc Ile		432
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													cct Pro		816
													cac His		864
													aaa Lys		912
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<sup>&</sup>lt;211> 600

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Erwinia rhapontici

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Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg 390 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 405 Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu Val Lys Gly Phe 420 425 Trp Gln Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Glu Glu Phe Leu 440 Gln Asn Val Arg Gln Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asp Ala Ser Lys Asn Ala Gly Phe Thr Ser Gly Thr Pro Trp Leu 470 Lys Ile Asn Pro Asn Tyr Lys Glu Ile Asn Ser Ala Asp Gln Ile Asn 490 Asn Pro Asn Ser Val Phe Asn Tyr Tyr Arg Lys Leu Ile Asn Ile Arg 500 505 His Asp Ile Pro Ala Leu Thr Tyr Gly Ser Tyr Ile Asp Leu Asp Pro Asp Asn Asn Ser Val Tyr Ala Tyr Thr Arg Thr Leu Gly Ala Glu Lys 535 Tyr Leu Val Val Ile Asn Phe Lys Glu Glu Val Met His Tyr Thr Leu 550 555 Pro Gly Asp Leu Ser Ile Asn Lys Val Ile Thr Glu Asn Asn Ser His 565 Thr Ile Val Asn Lys Asn Asp Arg Gln Leu Arg Leu Glu Pro Trp Gln . 585 Ser Gly Ile Tyr Lys Leu Asn Pro 595 600 <210> 7 <211> 1803 <212> DNA <213> Protaminobacter rubrum <220> <221> CDS <222> (1)..(1800) <223> coding for sucrose isomerase <400> 7 atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca 48 Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr tca tta tgc atc tca tgc cag caa gcc ttc ggt acg caa caa ccc ttg 96 Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu 25 ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp aag gag gct gtt ttt tat cag gtg tat ccg cgc tcc ttt aaa gac acc 192 Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr

						_							
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							tgg Trp						288
	-	_	_	_		-	ata Ile	_	_		_		336
							ttt Phe						384
•							att Ile						432
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•							aaa Lys						528
							ggt Gly						576
				_		_	cac His			_			624
							gtc Val						672
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			Lys				tat Tyr						816
							gag Glu					tac. Tyr	864
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							ctg Leu 315						960
							gat Asp						1008

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		gaa Glu								1104
		gct Ala	Val							1152
		gct Ala								1200
		att Ile 405								1248
		att Ile								1296
		gtt Val							ttg į Leu	1344
		ctg Leu								1392
		aaa Lys								1440
		aac Asn 485								1488
		gta Val								1536
		gca Ala								1584
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Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp 375 380 Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg 385 390 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 410 Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 420 425 Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu 440 Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe 470 475 Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Thr 485 490 Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg 505 His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro 520 Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys 535 Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys Leu 555 Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser Lys 570 Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln 585 590 · Ser Gly Val Tyr Lys Leu Asn Gln <210> 9 <211> 1794 <212> DNA <213> Enterobacter sp. <220> <221> CDS <222> (1)...(1791) <223> coding for sucrose isomerase atg tct ttt gtt acg cta cgt acc ggg gtg gct gtc gcg ctg tca tct 48 Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser . 10 ttg ata ata agt ctg gcc tgc ccg gct gtc agt gct gca cca tcc ttg 96 Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu aat cag gat att cac gtt caa aag gaa agt gaa tat cct gca tgg tgg Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp 35 40

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tat Tyr	ctg Leu	aaa Lys	tcg Ser	ctc Leu 85	ggt Gly	att Ile	gac Asp	gct Ala	atc Ile 90	tgg Trp	atc Ile	aat Asn	ccc Pro	cat His 95	tac Tyr	288
Asp	Ser	Pro	Asn 100	Thr	gat Asp	Asn	Gly	Tyr 105	Asp	Ile	Ser	Asn	Tyr 110	Arg	Gln	336
ata Ile	atg Met	aaa Lys 115	gag Glu	tat Tyr	ggc Gly	aca Thr	atg Met 120	gag Glu	gat Asp	ttt Phe	gat Asp	agc Ser 125	ctt Leu	gtt Val	gcc Ala	384
Glu	Met 130	Lys	Ĺys	Arg	aat Asn	Met 135	Arg	Leu	Met	Ile	Asp 140	Val	Val	Ile	Asn	432
cat His 145	acc Thr	agt Ser	gat Asp	caa Gln	cac His 150	ccg Pro	tgg Trp	ttt Phe	att Ile	cag Gln 155	agt Ser	aaa Lys	agc Ser	gat Asp	aaa Lys 160	480
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cag Gln	cca Pro	cct Pro	aat Asn 180	aat Asn	tac Tyr	ccc Pro	tca Ser	ttt Phe 185	ttc Phe	ggc Gly	ggc Gly	tcg Ser	gca Ala 190	tgg Trp	caa Gln	576
aaa Lys	gat Asp	gca Ala 195	aag Lys	tca Ser	gga Gly	cag Gln	tac Tyr 200	tat Tyr	tta Leu	cac His	tat Tyr	ttt Phe 205	gcc <sup>°</sup> Ala	aga Arg	cag Gln	624
Gln	Pro 210	Asp	Leu	Asn	tgg Trp	Asp 215	Asn	Pro	Lys	Val	Arg 220	Glu	Asp	Leu	Tyr	672
Ala 225	Met	Leu	Arg	Phe	tgg Trp 230	Leu	Asp	Lys	Gly	Val 235	Ser	Gly	Met	Arg	Phe 240	720
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gat Asp	gtg Val 290	gcc Ala	acc <sup>.</sup> Thr	gcg Ala	ggt Gly	gaa Glu. 295	att Ile	ttt <sup>.</sup> Phe	ggc Gly	gtc Val	ccg Pro- 300	ctg Leu	gat. Asp	cgt. Arg	tcg Ser	912
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										atc Ile			1056
										ttc Phe			1104
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										gga Gly			1440
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										cag Gln			1584
_	_			_		_		_	_	ctg Leu 540		 _	1632
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1794

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Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp 345 Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg 390 . 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 405 Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 425 Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe 470 475 His Ile Asn Pro Asn Tyr Val Glu Ile Asn Xaa Glu Arg Glu Glu Thr 490 Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg 505 His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro 515 520 Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu 555 Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln 565 570 Gly Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala Gly 580 585 Ala Tyr Lys Leu Arg 595 <210> 11 <211> 1803 <212> DNA <213> Serratia plymuthica <220> <221> CDS <222> (1)..(1800) <223> coding for sucrose isomerase atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca. 48 Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr 10 tca tta age gte tca tge cag caa gee tta ggt acg caa caa eee ttg Ser Leu Ser Val Ser Cys Gln Gln Ala Leu Gly Thr Gln Gln Pro Leu 20.

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Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys As 50	
Asn Gly Asp Gly Ile Gly Asp Ile Lys Gly Ile Ile Glu Lys Lee 65 70 75  tat tta aaa gct ttg ggg att gat gcc att tgg atc aac cca ca Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro Hi 85 90 90 90 90 90 90 90 90 90 90 90 90 90	
Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro Hi 85 90 90  gac tcc ccg aac acg gat aat ggt tac gat ata cgt gat tat cg Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Ar 100 105 110  atc atg aaa gaa tat ggc acg atg gag gat ttt gac cgc ctg at Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Il 115 120 125  gaa atg aaa aaa cgt aac atg cgg ttg atg att gat gtg gtc at Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Il 130 135 140  cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc ag	
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg 100 105 110 110 110 110 110 110 110 110	
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Il 115 120 125  gaa atg aaa aaa cgt aac atg cgg ttg atg att gat gtg gtc at Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Il 130 135 140  cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc ag	
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gat acg gta gcg acc tac tca aaa att ccg gac ttc cca aat ct Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Le 245 250 250	eu Thr
Caa caa cag ctg aag aat ttt gca gct gag tat acc aag ggc co Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pr 260 265 270	
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<223> Description of the artificial sequence: coding for fusion protein of signal peptide from proteinase inhibitor I and sucrose isomerase from Erwinia rhapontici

<220>

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<222> (24)..(1835)

25

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 Ala Tyr Leu Leu Ile Val Leu Gly Leu Leu Val Leu Val Ser Ala Met
 gag cat gtt gat gcg aag gct tgc acc gaa ttg ggg atc ctc acc gtt
                                                                     149
 Glu His Val Asp Ala Lys Ala Cys Thr Glu Leu Gly Ile Leu Thr Val
. cag caa tca aat gcc ctg ccc aca tgg tgg aag cag gct gtt ttt tat
                                                                     197
 Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp Lys Gln Ala Val Phe Tyr
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 cag gta tat cca cgc tca ttt aaa gat acg aat ggg gat ggc att ggg
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 Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr Asn Gly Asp Gly Ile Gly
 gat tta aac ggt att att gag aat tta gac tat ctg aag aaa ctg ggt
                                                                     293
 Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp Tyr Leu Lys Lys Leu Gly
                       80
 att gat gcg att tgg atc aat cca cat tac gat tcg ccg aat acg gat
                                                                     341
 Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp
                                      100
 aat ggt tat gac atc cgg gat tac cgt aag ata atg aaa gaa tac ggt
 Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys Ile Met Lys Glu Tyr Gly
              110
 acg atg gaa gac ttt gac cgt ctt att tca gaa atg aag aaa cgc aat
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 Thr Met Glu Asp Phe Asp Arg Leu Ile Ser Glu Met Lys Lys Arg Asn
 atg cgt ttg atg att gat att gtt atc aac cac acc agc gat cag cat
                                                                     485
 Met Arg Leu Met Ile Asp Ile Val Ile Asn His Thr Ser Asp Gln His
                          145
 gcc tgg ttt gtt cag agc aaa tcg ggt aag aac aac ccc tac agg gac
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 Ala Trp Phe Val Gln Ser Lys Ser Gly Lys Asn Asn Pro Tyr Arg Asp
 tat tac ttc tgg cgt gac ggt aag gat ggc cat gcc ccc aat aac tat
                                                                     581
 Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly His Ala Pro Asn Asn Tyr
 ccc tcc ttc ttc ggt ggc tca gcc tgg gaa aaa gac gat aaa tca ggc
                                                                     629
 Pro Ser Phe Phe Gly Gly Ser Ala Trp Glu Lys Asp Asp Lys Ser Gly
             190
 cag tat tac ctc cat tac ttt gcc aaa cag caa ccc gac ctc aac tgg
                                                                     677
 Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln Gln Pro Asp Leu Asn Trp
         205
                              210
```

								. •						
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											tta Leu			821
											tac Tyr 280			869
											act Thr			917
-				_	-		_		_		ttc Phe	-	_	965
_	_	_					-		_	_	atc Ile			1013
											acc Thr			1061
											gga Gly 360			1109
											cgc Arg			1157
											gcg Ala			1205
											ttt Phe			1253
											aaa Lys			1301
											tac Tyr 440			1349
											cgc Arg			1397
											agc Ser			1445
											ccc Pro			1493

aaa Lys	gaa Glu	atc Ile	aac Asn	agc Ser 495	gca Ala	gat Asp	cag Gln	att Ile	aat Asn 500	aat Asn	cca Pro	aat Asn	tcc Ser	gta Val 505	ttt Phe	1541
aac Asn	tat Tyr	tat Tyr	aga Arg 510	aag Lys	ctg Leu	att 'Ile	aac Asn	att Ile 515	cgc Arg	cat His	gac Asp	atc Ile	cct Pro 520	gcc Ala	ttg Leu	1589
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Ala	tac Tyr 540	Thr	Arg	Thr	Leu	Gly 545	Ala	Glu	Lys	Tyr	Leu 550	Val	Val	Ile	Asn	1685
Phe 555	aaa Lys	Glu	Glu	Val	Met 560	His	Tyr	Thr	Leu	Pro 565	Gly	Asp	Leu	Ser	Ile 570	1733
Asn	aag Lys	Val	Ile	Thr 575	Glu	Asn	Asn	Ser	His 580	Thr	Ile	Val	Asn	Lys 585	Asn	1781
gac Asp	agg Arg	caa Gln	ctc Leu 590	cgt Arg	ctt Leu	gaa Glu	ccc Pro	tgg Trp 595	cag Gln	tcg Ser	ggc Gly	att Ile	tat Tyr 600	aaa Lys	ctt Leu	1829
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	3> De fi	escr:	iption	on o	then of	art sign	nal p	ept:	ide i	Erom	prot	teina	ase	r		•
	3> De fu in	escr: usion nhib:	iption	on o: oteir I ar	then of	art sign	nal p	ept:	ide i	Erom	prot	teina	ase	r	•	
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Lys	Ser	Gly	Lys	Asn 165	Asn	Pro	Tyr	Arg	Asp 170	Tyr	Tyr	Phe	Trp	Arg 175	Asp
Gly	Lys	Asp	Gly 180	His	Ala	Pro	Asn	Asn 185	Tyr	Pro	Ser	Phe	Phe 190	Gly	Gly
Ser	Ala	Trp 195	Glu	Lys	Asp	Asp	Lys 200	Ser	Gly	Gln	Tyr	Tyr 205	Leu	His	Tyr
Phe	Ala 210	Lys	Gln	Gln	Pro	Asp 215	Leu	Asn	Trp	Asp	Asn 220	Pro	Lys	Val	Arg
Gln 225	Asp	Leu	Tyr	Asp	Met 230	Leu	Arg	Phe	Trp	Leu 235	Asp	Lys	Gly	Val	Ser 240
Gly	Leu	Arg	Phe	Asp 245	Thr	Val	Ala	Thr	Tyr 250	Ser	Lys	Ile	Pro	Asn 255	Phe
Pro	Asp	Leu	Ser 260	Gln	Gln	Gln	Leu	Lys 265	Asn	Phe	Ala	Glu	Glu 270	Tyr	Thr
Lyş	Gly	Pro 275		Ile	His	Asp	Tyr 280	Val	Asn	Glu	Met	Asn 285	Arg	Glu	Val
<u>L</u> eu	Ser 290	His	Tyr	Asp	Ile	Ala 295	Thr	Ala	Gly	Glu	Ile 300	Phe	Gly	Val	Pro
Leu 305	Asp	Lys	Ser	Ile	Lys 310	Phe	Phe	Asp	Arg	Arg 315	Arg	Asn	Glu	Leu	Asn 320
Ile	Ala	Phe	Thr	Phe 325	Asp	Leu	Ile	Arg	Leu 330	Asp	Arg	Asp	Ala	Asp 335	Gļu
Arg	Trp	Arg	Arg 340	Lys	Asp	Trp	Thr	Leu 345	Ser	Gln	Phe	Arg	Lys 350	Ile	Val
Asp	Lys	Val 355	Asp	Gln	Thr	Ala	Gly 360	Glu	Tyr	Gly	Trp	Asn 365	Ala	Phe	Phe
	370				Asn	375					380				
385			•		Glu 390	•	•			395					4.00
				405	Thr				410					415	_
			420	•	Phe			425					430		
		435			Gln		440				•	445			
	450				Asn	455					460				
465					Asp 470					475					480
Thr	Pro	Trp	Leu	Lys 485	Ile	Asn	Pro	Asn	Tyr 490	Lys	Glu	Ile	Asn	Ser 495	Ala
			500		Pro			505					510		
		515	•		Asp		520					525			
Asp	Leu 530	Asp	Pro	Asp	Asn	Asn 535	Ser	Val	Tyr	Ala	Tyr 540	Thr	Arg	Thr	Leu

29

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Gly 545	Ala	Glu	Lys	Tyr	Leu 550	Val	Val	Ile	Asn	Phe 555		Glu	Glu	Val	Met 560	
His	Tyr	Thr	Leu	Pro 565		Asp	Leu	Ser	Ile 570		Lys	Val	Ile	Thr 575		
		Ser	580	ı				5 <b>85</b>					Leu 590		Leu	
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acc Thr	Gly	gtg Val 10	gct Ala	gtc Val	gcg Ala	ctg Leu	tca Ser 15	tct Ser	ttg Leu	ata Ile	ata Ile	agt Ser 20	Leu	gcc Ala	tgc Cys	282
ccg Pro	gct Ala 25	gtc Val	agt Ser	gct Ala	gca Ala	cca Pro 30	tcc Ser	ttg Leu	aat Asn	cag Gln	gat Asp 35	att Ile	cac His	gtt Val	caa Gln	330
Lys 40	Glu	agt Ser	Glu	Tyr	Pro 45	Ala	Trp	Trp	Lys	Glu 50	Ala	Val	Phe	Tyr	Gln 55	378
Ile	Tyr	cct Pro	Arg	Ser 60	Phe	Lys	Asp	Thr	Asn 65	Asp.	Asp	Gly	Ile	Gly 70	Asp	426
Ile	Arg	ggt Gly	Tle 75	Ile	Glu	Lys	Leu	Asp 80	Tyr	Leu	Lys	Ser	Leu 85	Gly	Ile	474
Asp	Ala	atc Ile 90	Trp	Ile	Asn	Pro	His 95	Tyr	Asp	Ser	Pro	Asn 100	Thr	Asp	Asn	522
ggc	tat Tyr 105	gac Asp	atc <sup>.</sup> Ile	agt Ser	aat Asn	tat Tyr 110	cgt Arg	cag Gl'n	ata Ile	atg Met	aaa Lys 115	gag Glu	tat Tyr	ggc Gly	aca Thr	570
atg Met 120	gag Glu	gat Asp	ttt. Phe	gat Asp	agc Ser 125	ctt Leu	gtt Val	gcc: Ala	gaa Glu	atg Met 130	aaa L <b>ys</b>	aaa Lys	cga Arg	aat Asn	atg Met 135	618
cgc Arg	tta Leu	atg Met	atc <sup>.</sup> Ile	gac Asp 140	gtg Val	gtc Val	att Ile	aac: Asn	cat His 145	acc Thr	agt Ser	gat Asp	caa Gln	cac His 150	ccg <sup>-</sup> Pro	666

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Trp	ttt Phe	att	Caq Glr 155	ı Ser	aaa Lys	ago Ser	gat Asp	aaa Lys 160	Asn	aac Asn	cct Pro	tat Tyr	cgt Arg 165	Asp	tat Tyr	714
tat Tyr	tto Phe	tgg Trp	Arc	gac J Asp	gga Gly	aaa Lys	gat Asp 175	Asn	caç Glr	r cca	cct Pro	aat Asn 180	Asn	tac Tyr	ccc Pro	762
tca Ser	ttt Phe 185	: Pue	ggc Gly	ggc Gly	tcg Ser	gca Ala 190	Trp	caa Gln	aaa Lys	gat Asp	gca Ala	Lys	tca Ser	gga Gly	cag Gln	810
200	туг	Leu	HIS	Tyr	205	Ala	Arg	Gln	Gln	210	Asp	Leu	Asn	Trp	gat Asp 215	858
ASI	PIC	rys	vaı	220	Glu	Asp	Leu	Tyr	Ala 225	. Met	Leu	Arg	Phe	Trp 230		906
Asp	rås	GIA	235	Ser	Gly	Met	Arg	Phe 240	Asp	Thr	Val	Ala	Thr 245	Tyr	tcc Ser	954
aaa Lys	atc Ile	ccg Pro 250	GTĀ	ttt Phe	Pro	aat Asn	ctg Leu 255	aca Thr	cct Pro	gaa Glu	caa Gln	cag Gln 260	aaa Lys	aat Asn	ttt Phe	1002
gct Ala	gaa Glu 265	GIn	tac Tyr	acc Thr	atg Met	999 Gly 270	cct Pro	aat Asn	att Ile	cat His	cga Arg 275	tac Tyr	att Ile	cag Gln	gaa Glu	.1050
280	Asn	Arg	Lys	Val	Leu 285	Ser	cgg Arg	Tyr	Asp	Val 290	Ala	Thr	Ala	Gly	Glu 295	1098
116	Pne	СТĀ	val	300	Leu	Asp	cgt Arg	Ser	Ser 305	Gln	Phe	Phe	Asp	Arg 310	Arg	1146
cga Arg	cat His	gag Glu	ctg Leu 315	aat Asn	atg Met	gcg Ala	ttt Phe	atg Met 320	ttt Phe	gac Asp	ctc Leu	att Ile	cgt Arg 325	ctc Leu	gat Asp	1194
Arg	ASP	330	Asn	GIu	Arg	Trp	cgt Arg 335	His	Lys	Ser	Trp	Ser 340	Leu	Ser	Gln	1242
Pne	345	GIN	TTE	TTE	Ser	Lys 350	atg Met	Asp	Val	Thr	Val 355	Gly	Lys	Tyr	Gly	1290
360	ASI	Thr	Pne	Phe	165	Asp	aac Asn	His	Asp	Asn 37.0	Pro	Arg	Ala	Val.	Ser 375	1338
cac His	ttc Phe	ggg	gat Asp	gac Asp 380	agg Arg	ccg Pro	caa Gln	tgg Trp	cgg Arg 385	gag Glu	gcg Ala	tcg Ser	gct. Ala	aag Lys 390	gca Ala	1386
Leu	АТА	THE	395	Thr	Leu	Thr	cag Gln.	Arg 400	Aľa	Thr	Pro	Phe	11e 405	Tyr	Gln	1434
ggt Gly	tca Ser	gag Glu 410	ctg Leu	gga Gly	atg Met	act Thr	aat Asn 415	tat Tyr	ccc Pro	ttc Phe	agg <sup>.</sup> Arg	caa GIn 420	ctc Leu	aac: Asn.	gaa Glu	1482

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cgc gat aac Arg Asp Asn	agc aga ac Ser Arg Th 460	a cct ttc Pro Phe	cag tgg Gln Trp 465	aat gad Asn Asp	acc ctg Thr Leu	aat gct Asn Ala 470	1626
ggt ttt act Gly Phe Thr	cgc gga aa Arg Gly Ly 475	g ccg tgg s Pro Trp	ttt cac Phe His 480	atc aac	cca aac Pro Asn 485	tat gtg Tyr Val	1674
gag atc aac Glu Ile Asn 490	Ala Glu Ar	J Glu Glu 495	Thr Arg	Glu Asp	Ser Val	Leu Asn	1722
tac tat aaa Tyr Tyr Lys 505	Lys Met Ile	Gln Leu 510	Arg His	His Ile	Pro Ala	Leu Val	1770
tat ggc gcc Tyr Gly Ala 520	Tyr Gln Asy	Leu Asn	Pro Gln	Asp Asn 530	Thr Val	Tyr Ala 535	1818
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gaa gtg gtc Glu Val Val 570	att gat act	cag cag Gln Gln 575	cag gcg Gln Ala	gct gcg Ala Ala	ccg cac Pro His 580	agc aca Ser Thr	1962
tcc ctg tca Ser Leu Ser 585	ttg agc ccc Leu Ser Pro	tgg cag Trp Gln 590	gca ggt Ala Gly	gtg tat Val Tyr 595	Lys Leu	cgg Arg	2007
taatcacctg	•	•					
actgctgtgc 1					· ·		
aggcattgtc a							
cccctgaaa q							
catcttatca a							
tgcgcctgaa g							
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Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln 100 Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala 120 Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys 150 Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn 170 Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln 185 Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe 235 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr 245 Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Gly Pro Asn 265 Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr 280 Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser 290 Ser Gln Phe Phe Asp Arg Arg His Glu Leu Asn Met Ala Phe Met 310 315 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His 330 Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp 345 Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp 3.75 Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 410

Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 420 425 Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu 440 445 Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe 470 . His Ile Asn Pro Asn Tyr Val Glu Ile Asn Ala Glu Arg Glu Glu Thr 485 490 Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg 500 505 His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro 520 Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg 535 Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu 550 555 Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln Ala Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala 585 Gly Val Tyr Lys Leu Arg 595 <210> 17 <211> 1797 <212> DNA <213> Klebsiella sp. <220> <221> CDS <222> (1)..(1794) <223> coding for sucrose isomerase atg tot tit git acg cta cgt acc ggg gtg gct gtc gcg ctg tca tot 48 Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser ttg ata ata agt ctg gcc tgc ccg gct gtc agt gct gca cca tcc ttg Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu 20 aat cag gat att cac gtt caa aag gaa agt gaa tat cct gca tgg tgg Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp aaa gaa gct gtt ttt tat cag atc tat cct cgc tca ttt aaa gac acc 192. Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr 55 aat gat gat ggc att ggc gat att cgc ggt att att gaa aag ctg gac 2.40 Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp tat ctg aaa tcg ctc ggt att gac gct atc tgg atc aat ccc cat tac 288. Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr

	•									•	<i>,</i> =						
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•	ata Ile	atg Met	aaa Lys 115	gag Glu	tat Tyr	ggc Gly	aca Thr	atg Met 120	gag Glu	gat Asp	ttt Phe	gat Asp	agc Ser 125	ctt Leu	gtt Val	gcc Ala	384
	gaa Glu	atg Met 130	aaa Lys	aaa Lys	cga Arg	aat Asn	atg Met 135	cgc Arg	tta Leu	atg Met	atc Ile	gac Asp 140	gtg Val	gtc Val	att Ile	aac Asn	432
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Lys

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ctt Leu	aac Asn	gaa Glu 35	aag Lys	agt Ser	atc Ile	gaa Glu	cag Gln 40	tcg Ser	aaa Lys	acc	ata Ile	cct Pro 45	aaa Lys	tgg Trp	tgg Trp	144
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gac Asp	tcc Ser	ccg Pro	aac Asn 100	acg Thr	gat Asp	aat Asn	ggt Gly	tac Tyr 105	gat Asp	ata Ile	cgt Arg	gat Asp	tat Tyr 110	cga Arg	aaa Lys	336
atc Ile	atg Met	aaa Lys 115	gaa Glu	tat Tyr	ggc Gly	acg Thr	atg Met 120	gag Glu	gat	ttt Phe	gac Asp	cgc Arg 125	ctg Leu	att Ile	tct Ser	384
gaa Glu	atg Met 130	aaa Lys	aaa Lys	cgt Arg	aac Asn	atg Met 135	cgg Arg	ttg Leu	atg Met	att Ile	gat Asp 140	gtg Val	gtc Val	atc Ile	aac Asn	432
cac His 145	acc Thr	agc Ser	gat Asp	caa Gln	aac Asn 150	gaa Glu	tgg Trp	ttt Phe	gtt Val	aaa Lys 155	agt Ser	aaa Lys	agc Ser	agt Ser	aag Lys 160	480
gat Asp	aat Asn	cct Pro	tat Tyr	cgt Arg 165	ggc Gly	tat Tyr	tac Tyr	ttc Phe	tgg Trp 170	aaa Lys	gat Asp	gct Ala	aaa Lys	gaa GIu 175	gl <sup>à</sup> aaa	528
cag Gln	gcg Ala	cct Pro	aat Asn 180	aat Asn	tac Tyr	cct Pro	tca Ser	ttc Phe 185	ttt. Phe	ggt Gly	ggc Gly	tcg Ser	gcg Ala 190	tgg Trp	caa Gln	5.7.6:
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	atg					tta		aaa Lys			tct					720
								att Ile								768
								gct Ala 265								816
								aat Asn								864
gac Asp	att Ile 290	gcc Ala	act Thr	gcc Ala	ggt Gly	gaa Glu 295	atc Ile	ttt Phe	ggc Gly	gta Val	ccc Pro 300	ttg Leu	gat Asp	caa Gln	tcg Ser	912
ata Ile 305	aaa Lys	ttc Phe	ttc Phe	gat Asp	cgc Arg 310	cgt Arg	cgc Arg	gat Asp	gag Glu	ctg Leu 315	aac Asn	atc Ile	gca Ala	ttt Phe	acc Thr 320	960
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caa Gln	aat Asn 450	gta Val	cgc Arg	ctg Leu	acg Thr	agc Ser 455	agg Arg	gat Asp	aac Asn	agc Ser	cgg Arg 460	aca Thr	ccg Pro	ttc Phe	caa Gln	1392
tgg Trp 465	gat Asp	acg Thr	agc Ser	aaa Lys	aat Asn 470	gca Ala	gga Gly	ttc Phe	acg Thr	agc Ser 475	gga Gly	aaa Lys	cct Pro	tgg Trp	ttc Phe 480	1440

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cag Gln	ccc Pro	gac Asp	tcg Ser 500	gta Val	ttt Phe	aat Asn	tat Tyr	tat Tyr 505	cgt Arg	cag Gln	ttg Leu	atc Ile	aag Lys 510	ata Ile	agg Arg	1536
cat His	aac Asn	atc Ile 515	ccg Pro	gca Ala	ctg Leu	acc Thr	tat Tyr 520	ggc Gly	aca Thr	tac Tyr	acc Thr	gat Asp 525	ttg Leu	gat Asp	cct Pro	1584
gca Ala	aat Asn 530	gat Asp	tcg Ser	gtc Val	tac Tyr	gcc Ala 535	tat Tyr	aca Thr	cgc Arg	agc Ser	ctt Leu 540	ggg Gly	gcg Ala	gaa Glu	aaa Lys	1632
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	305					310					315					320	
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	385					Lys 390					395					400	
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		•		420		Asp			425					430			
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		450		,		Thr	455					460					
-	400					Asn 470					475					480	
					485	Tyr			•	490					495		
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			515			Leu		520					525				
		530					535					540					
T 5	'yr 45	Leu	Val	Val	Val	Asn´: 550	Phe (	Gln	Glu	Gln	Val. 555	Met	Arg	туг	Lys	Leu 560	

50

Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Glu Ser Asn Ser Lys 565 570 Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln

585 590

Ser Gly Val Tyr Lys Leu Asn Gln 595